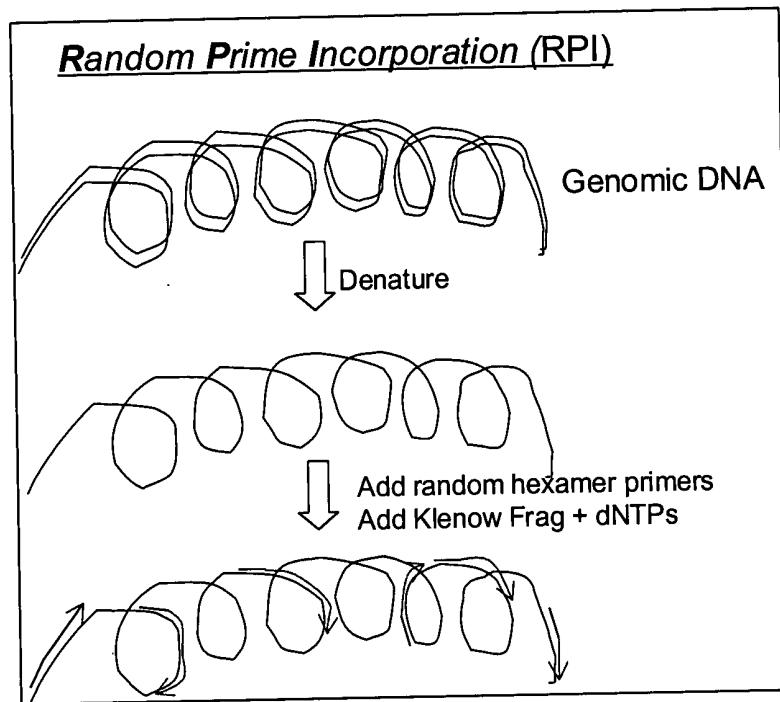


Figure 1



2/8

Figure 2

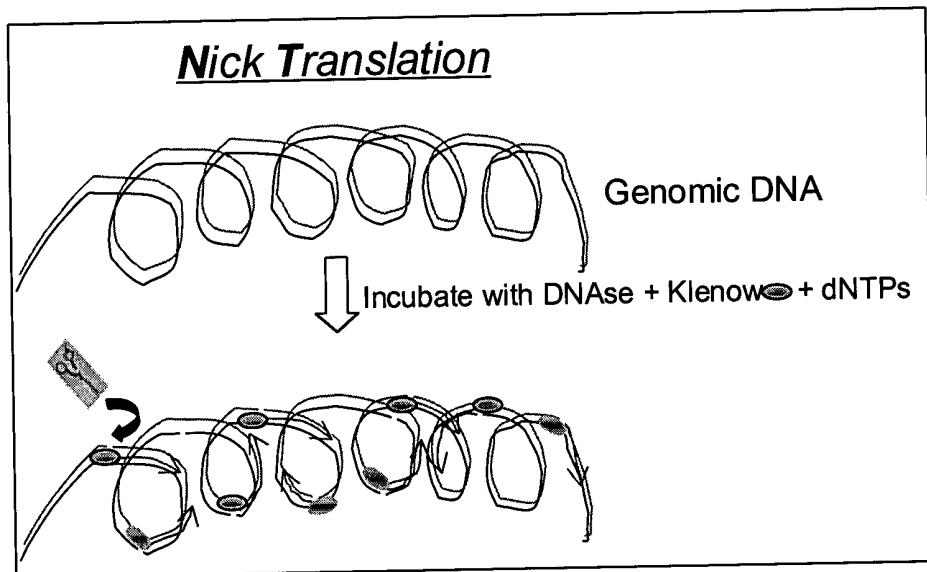


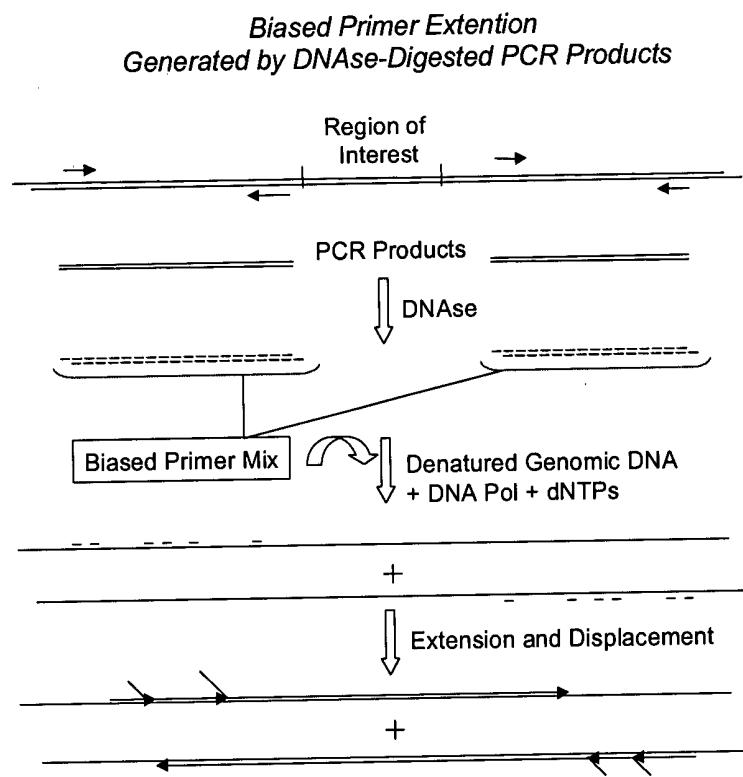
Figure 3

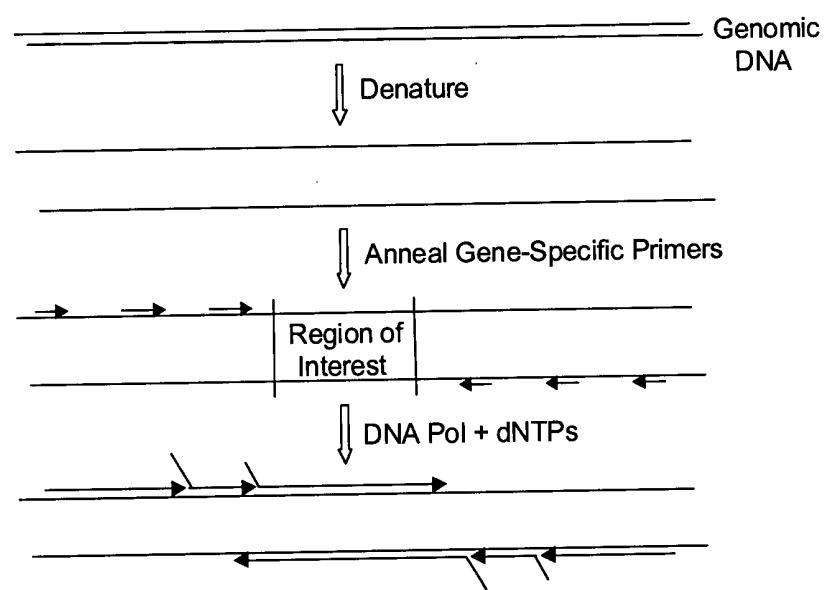
Figure 4*Gene-Specific Primer Extension using DNA Polymerase*

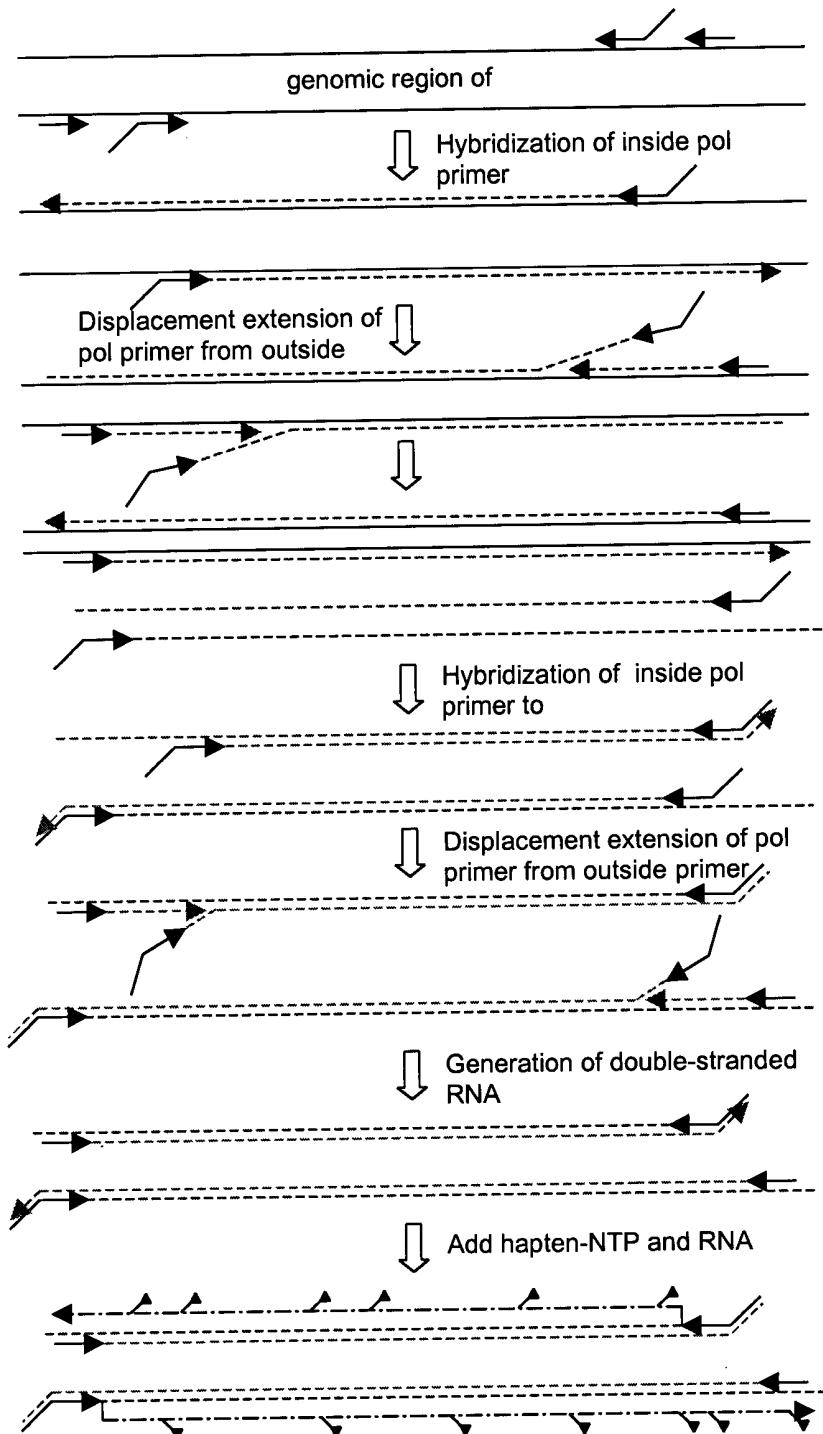
Figure 5**Extension Displacement Transcription Incorporation (EDTI)**

Figure 6

1. 'A' Allele, CYP2D6*3, A2637 deletion, Frame shift resulting in zero enzyme activity

2637

5'- G C T A A C T G A G C A C A G G A T G A C C -3' NH2	CYPwt(+)A2624,22mer,54%GC, Tm=63-64C
5'- G C T A A C T G A G C A C A G G A T G A C C (A)30-3' NH2	CYPwt(+)A2624(A)30-3'NH2
5'- C T A A C T G A G C A C A G G A T G A C C (A)30-3' NH2	CYPwt(+)A2625(A)30-3'NH2
5'- C T A A C T G A G C A C A G G A T G A C (A)30-3' NH2	CYPwt(-)A2625b(A)30-3'NH2
5'- G C T A A C T G A G C A C - G G A T G A C C -3' NH2	CYPmut(+)A2624,21mer,57%GC, Tm=61-63C
5'- G C T A A C T G A G C A C - G G A T G A C C (A)30-3' NH2	CYPmut(+)A2624(A)30-3'NH2
5'- C T A A C T G A G C A C - G G A T G A C C (A)30-3' NH2	CYPmut(+)A2625(A)30-3'NH2
5'- C T A A C T G A G C A C - G G A T G A C (A)30-3' NH2	CYPmut(+)A2625b(A)30-3'NH2
5'- C T A A C T G A G C A C - G G A T G A C (A)30-3' NH2	Wild Type (+)
5'- G C T G G A T G A G C T G C T A A C T G A G C A C - G G A T G A C C T G G G A C C C A G C C C A G C C C -3'	Mut (-)
5'- G C T G G A T G A G C T G C T A A C T G A G C A C - G G A T G A C C T G G G A C C C A G C C C A G C C C -3'	Mut (+)

2. 'B' Allele, CYP2D6*4, G1934A, Splicing defect resulting in zero enzyme activity

A. wt Probe - CYPwt(-)B1922 (C/A to mut at base 5) & CYPmut(+)B1922 (A/C to mut at base 13)

1934

NH2 3'- G A G G G T G G G G G T C C T G C -5'	CYPwt(-)B1922,17mer,76%GC, Tm=66C
5'- C T C C C A C C C C C A G G A C G -3' NH2	CYPwt(+)B1922- Target
5'- C T C C C A C C C C C A A G A C G -3' NH2	CYPmut(+)B1922,17mer,71%GC, Tm=58-60C
-1909 NH2 3'- G A G G G T G G G G G T T C T G C -5'	CYPmut(-)B1922- Target
5'- C C C T T A C C C G C A T C T C C C A C C C C C A G G A C G C C C C T T C G C C C C A A C G G T C T -3'	Wild Type (+)
5'- C C C T T A C C C G C A T C T C C C A C C C C C A A G A C G C C C C T T C G C C C C A A C G G T C T -3'	Mut (+)

B. CYPwt(-)B1930 (C/A to mut at base 13) and CYPmut(+)B1930 (A/C to wt at base 5)

NH2 3'- G G G T C C T G C G G G G A A A G -5'	CYPwt(-)B1930,17mer,71%GC, Tm=56C
NH2 3'-(A)30 G G G T C C T G C G G G G A A A G -5'	CYPwt(-)B1930(A)30-3'NH2
5'- C C C A A G A C G C C C C T T T C -3' NH2	CYPmut(+)B1930,17mer,65%GC, Tm=54C
5'- C C C A A G A C G C C C C T T T C (A)30-3' NH2	CYPmut(+)B1930(A)30-3'NH2

|-1909

5'- C C C T T A C C C G C A T C T C C C A C C C C C A G G A C G C C C C T T C G C C C C A A C G G T C T -3'	Wild Type (+)
5'- C C C T T A C C C G C A T C T C C C A C C C C C A A G A C G C C C C T T C G C C C C A A C G G T C T -3'	Mut (+)

3. 'C' Allele, CYP2D6*9, G2702-A2704 deletion, decreased enzyme activity

|-2702

5'- G C A G A G A T G G A G A A G G T G A G A G -3' NH2	CYPwt(+)C2691,22mer,55%GC, Tm=60C
5'- G C A G A G A T G G A G A A G G T G A G A G (A)30-3' NH2	CYPwt(+)C2691(A)30-3'NH2
5'- C A G A G A T G G A G A A G G T G A G A G (A)30-3' NH2	CYPwt(+)C2692(A)30-3'NH2
5'- G C A G A G A T G G A - - - G G T G A G A G T G -3' NH2	CYPmut(+)C2691,21mer,57%GC, Tm=60C
5'- G C A G A G A T G G A - - - G G T G A G A G T G (A)30-3' NH2	CYPmut(+)C2691(A)30-3'NH2
5'- C A G A G A T G G A - - - G G T G A G A G T G (A)30-3' NH2	CYPmut(+)C2692(A)30-3'NH2
-2676 5'- C A G A G A T G G A - - - G G T G A G A G T G (A)30-3' NH2	Wild Type (-)
-3 5'- T G A C T C C G G A A G G A C C G T C T C A C C T C T T C C A C T C T C A C C G A C G G T G C C A C -5'	Mut (-)
-3 5'- T G A C T C C G G A A G G A C C G T C T C A C C T C T C A C C G A C G G T G C C A C -5'	Mut (+)

4. 'E' Allele, CYP2D6*7, A3023C, H324P amino acid change results in zero enzyme activity

A. wt Probe - CYPwt(-)E3009 (T/C to mut at base 5) & CYPmut(+)E3009 (C/A to wt at base 15)

3023

NH2 3'- C G A G T A C T A G G A T G T A G G C -5'	CYPwt(-)E3009,19mer,53%GC,Pred Tm=57
NH2 3'-(A)30 C G A G T A C T A G G A T G T A G G C -5'	CYPwt(-)E3009(A)30-3'NH2
5'- G C T C A T G A T C C T A C C T C C G -3' NH2	CYPmut(+)-E3009,19mer,58%GC,Pred Tm=59C
5'- G C T C A T G A T C C T A C C T C C G (A)30-3' NH2	CYPmut(+)-E3009(A)30-3'NH2
-2998 5'- T G G G G C C T C C T G C T C A T G A T C C T A C A T C C G G A T G T G C A G C G T G A G C C C A T C -3'	Wild Type (+)
5'- T G G G G C C T C C T G C T C A T G A T C C T A C C T C C G G A T G T G C A G C G T G A G C C C A T C -3'	Mut (+)
5'- T G G G G C C T C C T G C T C A T G A T C C T A C C T C C G G A T G T G C A G C G T G A G C C C A T C -3'	-3038-Intron Start

B. CYPwt(-)E3018 (T/C to mut at base 14) and CYPmut(+)E3018 (C/T to wt at base 6)

NH2 3'- G G A T G T A G G C C T A C A C G T C -5'	CYPwt(-)E3018,19mer,58%GC, Tm=60
5'- C C T A C A T C C G G A T G T G C A G -3'	CYPwt(+)E3018- Target
5'- C C T A C C T C C G G A T G T G C A G -3' NH2	CYPmut(+)-E3018,19mer, 63%GC, Tm=62C
3'- G G A T G G A G G C C T A C A C G T C -5'	CYPmut(-)E3018- Target
-2998 5'- T G G G G C C T C C T G C T C A T G A T C C T A C A T C C G G A T G T G C A G C G T G A G C C C A T C -3'	Wild Type (+)
5'- T G G G G C C T C C T G C T C A T G A T C C T A C C T C C G G A T G T G C A G C G T G A G C C C A T C -3'	Mut (+)
5'- T G G G G C C T C C T G C T C A T G A T C C T A C C T C C G G A T G T G C A G C G T G A G C C C A T C -3'	-3038-Intron Start

5. 'G' Allele, CYP2D6*8, G1846T, Stop codon, zero enzyme activity

1846

5'- C A C T C C G G T G G G T G A T G G (A)30-3' NH2	CYPwt(+)G1840(A)30-3'NH2,18mer,67%GC, Tm=60
NH2 3'-(A)30 G T G A G G C C A C C C A C T A C C -5'	CYPwt(-)G1840(A)30-3'NH2
5'- C A C T C C T G T G G G T G A T G G (A)30-3' NH2	CYPmut(+)G1840(A)30-3'NH2,18mer,61%GC, Tm=57
5'- G T G C C G G C C T T C G C C A C T C C G G T G G G T G A T G G G A G A G G G C A C A A A G C G G G -3'	
5'- G T G C C G G C C T T C G C C A C T C C G G T G G G T G A T G G G A G A G G G C A C A A A G C G G G -3'	
Exon 3 end--1846	

6. 'I' Allele, CYP2D6*6, T1795 deletion, Frameshift resulting in zero enzyme activity

5'- GCTGGAGCAGTGGGTGAC - 3' NH2 CYPwt(+)-T1785,18mer,67%GC, Tm=59-61C
 5'- GCTGGAGCAGTGGGTGAC (A)30-3' NH2 CYPwt(+)-T1785(A)30-3'NH2
 5'- CTGGAGCAGTGGGTGAC (A)30-3' NH2 CYPwt(+)-T1786(A)30-3'NH2
 5'- GCTGGAGCAG - GGGTGAC - 3' NH2 CYPmut(-)-T1785,17mer,71%GC, Tm=58-60C
 5'- GCTGGAGCAG - GGGTGAC (A)30-3' NH2 CYPmut(-)-T1785(A)30-3'NH2
 5'- CTGGAGCAG - GGGTGAC (A)30-3' NH2 CYPmut(-)-T1786(A)30-3'NH2

|-1773

5'- GGGCAAGAACGTCGCTGGAGCAGTGGGTGACCGAGGAGGCCGCTGCTT - 3' Wild Type (+)
 5'- GGGCAAGAACGTCGCTGGAGCAG - GGGTGACCGAGGAGGCCGCTGCTT - 3' Mut (-)

7. 2D6/2D7/2D8 Controls - The 2D6/7/8 probes were designed in the 1600 region of the 2D6 gene. The purpose of the designs was to find region somewhere between the PCR primers where it would be easy to discriminate between 2D6 and its two pseudogenes, 2D7 and 2D8. The purpose of the designs is to demonstrate that the PCR amplicon is from the 2D6 gene, not one of the pseudogenes.

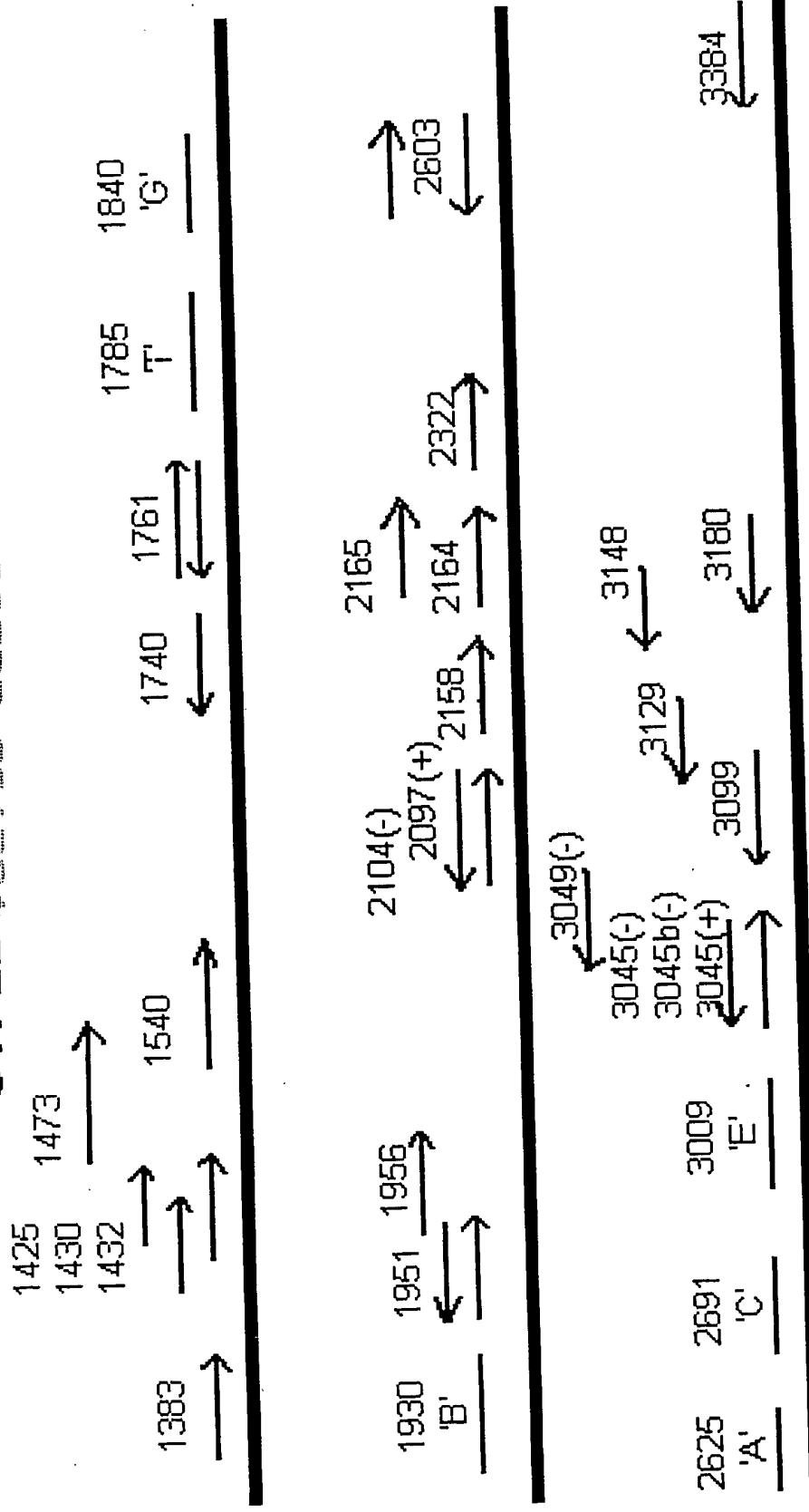
1603-1	5'- G A C C A G G G G G A G C - A T A G G (A)30-3' NH2	CYP2D6wt(+)	1607(A)30-3'NH2
	5'- G A C C T T G T G G A G C G C C A G (A)30-3' NH2	CYP2D7wt(+)	1607(A)30-3'NH2
	5'- G A C C A G G A A A A G C - A C A G G (A)30-3' NH2	CYP2D8wt(+)	1607(A)30-3'NH2
	5'- G A C C A G G A A A A G C - A C A G G G (A)30-3' NH2	CYP2D8wt(+)	1607b(A)30-3'NH2
	5'- G G G A G A C C A G G G G G A G C - A T A G G G T T G G A G T G G G T G G T -3'	2D6	(+)
	5'- G G G A G A C C T T G T G G A G C G C C A G G G T T G G A G T G G G T G G C -3'	2D7	(+)
	5'- G G G A G A C C A G G A A A A G C - A C A G G G T T G G A G T G G G C G G C -3'	2D8	(+)

8. Pos/Neg Control probes- These probes were designed as true positive and negative control probes. They consist of the same semi-random sequence, with the positive control probe having a 5' Biotin.

5' Biotin- A T C A T T C C A A T C A T C C A T A T C A T C (A)25'-3' NH2 CYP(+)ran(A)25-5'Biotin,3'NH2
 5'- A T C A T T C C A A T C A T C C A T A T C A T C (A)25'-3' NH2 CYP(+)ran(A)25-3'NH2

60
62
64
66
68
70
72
74
76
78
80

Figure 7

CYP2D6 Probes/Primers

CYP_{wt}(+)1383, CYP_{wt}(+)2097, CYP_{wt}(-)2104, and CYP_{wt}(-)3180 are published primer sequences.

1. Chen et al., Clinical Pharmacology and Therapeutics, Vol 60, 5:522-34
2. Heim M, Meyer UA. Lancet 1990; 336:529-32

CYP_{wt}(+)1540 and CYP_{wt}(-)3099 are primers obtained from Intek, referred to as MP3 and MP4 respectively.